

SEQUENCE LISTING

<110> Burgin, Alex B.
Stewart, Lance J.

<120> Use of Phosphorothiolate Polynucleotides
In Ligating Nucleic Acids

<130> P-RD 4806

<150> US 60/290,313
<151> 2001-05-10

<160> 19

<170> FastSEQ for Windows Version 4.0

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<213> Homo sapiens

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gtcaccggcg cttacactcgcc cttccggat ccccggtccgc cggcacaggc 180
cggttgcgcg tctgcgttc ccccacggcg cttcgccgtgc cggcggcgctc gtccctccgg 240
ggccgac atg agt ggg gac cac ctc cac aac gat tcc cag atc gaa gcg 288
Met Ser Gly Asp His Leu His Asn Asp Ser Gln Ile Glu Ala
1 5 10

gat ttc cga ttg aat gat tct cat aaa cac aaa gat aaa cac aaa gat 336
Asp Phe Arg Leu Asn Asp Ser His Lys His Lys Asp Lys His Lys Asp
15 20 25 30

cga gaa cac cgg cac aaa gaa cac aag aag gag aag gac cgg gaa aag 384
Arg Glu His Arg His Lys Glu His Lys Lys Glu Lys Asp Arg Glu Lys
35 40 45

tcc aag cat agc aac agt gaa cat aaa gat tct gaa aag aaa cac aaa 432
Ser Lys His Ser Asn Ser Glu His Lys Asp Ser Glu Lys Lys His Lys
50 55 60

gag aag gag aag acc aaa cac aaa gat gga agc tca gaa aag cat aaa 480
Glu Lys Glu Lys Thr Lys His Lys Asp Gly Ser Ser Glu Lys His Lys
65 70 75

gac aaa cat aaa gac aga gac aag gaa aaa cga aaa gag gaa aag gtt 528
Asp Lys His Lys Asp Arg Asp Lys Glu Lys Arg Lys Glu Glu Lys Val
80 85 90

cga gcc tct ggg gat gca aaa ata aag aag gag aag gaa aat ggc ttc 576
Arg Ala Ser Gly Asp Ala Lys Ile Lys Lys Glu Lys Asn Gly Phe
95 100 105 110

tct agt cca cca caa att aaa gat gaa cct gaa gat gat ggc tat ttt 624
Ser Ser Pro Pro Gln Ile Lys Asp Glu Pro Glu Asp Asp Gly Tyr Phe
115 120 125

gtt cct cct aaa gag gat ata aag cca tta aag aga cct cga gat gag 672
Val Pro Pro Lys Glu Asp Ile Lys Pro Leu Lys Arg Pro Arg Asp Glu
130 135 140

gat gat gct gat tat aaa cct aag aaa att aaa aca gaa gat acc aag 720
Asp Asp Ala Asp Tyr Lys Pro Lys Lys Ile Lys Thr Glu Asp Thr Lys
145 150 155

aag gag aag aaa aga aaa cta gaa gaa gag gat ggt aaa ttg aaa 768
Lys Glu Lys Lys Arg Lys Leu Glu Glu Glu Asp Gly Lys Leu Lys
160 165 170

aaa ccc aag aat aaa gat aaa gat aaa aaa gtt cct gag cca gat aac 816
Lys Pro Lys Asn Lys Asp Lys Asp Lys Lys Val Pro Glu Pro Asp Asn
175 180 185 190

aag aaa aag aag ccg aag aaa gaa gag aag cag aag tgg aaa ttg tgg 864
Lys Lys Lys Pro Lys Lys Glu Glu Gln Lys Trp Lys Trp Trp
195 200 205

gaa gaa gag cgc tat cct gaa ggc atc aag tgg aaa ttc cta gaa cat 912
Glu Glu Glu Arg Tyr Pro Glu Gly Ile Lys Trp Lys Phe Leu Glu His
210 215 220

aaa ggt cca gta ttt gcc cca cca tat gag cct ctt cca gag aat gtc 960
Lys Gly Pro Val Phe Ala Pro Pro Tyr Glu Pro Leu Pro Glu Asn Val
225 230 235

aag ttt tat tat gat ggt aaa gtc atg aag ctg agc ccc aaa gca gag 1008
Lys Phe Tyr Tyr Asp Gly Lys Val Met Lys Leu Ser Pro Lys Ala Glu
240 245 250

gaa gta gct acg ttc ttt gca aaa atg ctc gac cat gaa tat act acc 1056
Glu Val Ala Thr Phe Ala Lys Met Leu Asp His Glu Tyr Thr Thr
255 260 265 270

aag gaa ata ttt agg aaa aat ttc ttt aaa gac tgg aga aag gaa atg 1104
Lys Glu Ile Phe Arg Lys Asn Phe Phe Lys Asp Trp Arg Lys Glu Met
275 280 285

act aat gaa gag aag aat att atc acc aac cta agc aaa tgt gat ttt 1152

Thr Asn Glu Glu Lys Asn Ile Ile Thr Asn Leu Ser Lys Cys Asp Phe			
290	295	300	
acc cag atg agc cag tat ttc aaa gcc cag acg gaa gct cgg aaa cag			1200
Thr Gln Met Ser Gln Tyr Phe Lys Ala Gln Thr Glu Ala Arg Lys Gln			
305	310	315	
atg agc aag gaa gag aaa ctg aaa atc aaa gag gag aat gaa aaa tta			1248
Met Ser Lys Glu Glu Lys Leu Lys Ile Lys Glu Glu Asn Glu Lys Leu			
320	325	330	
ctg aaa gaa tat gga ttc tgt att atg gat aac cac aaa gag agg att			1296
Leu Lys Glu Tyr Gly Phe Cys Ile Met Asp Asn His Lys Glu Arg Ile			
335	340	345	350
gct aac ttc aag ata gag cct cct gga ctt ttc cgt ggc cgc ggc aac			1344
Ala Asn Phe Lys Ile Glu Pro Pro Gly Leu Phe Arg Gly Arg Gly Asn			
355	360	365	
cac ccc aag atg ggc atg ctg aag aga cga atc atg ccc gag gat ata			1392
His Pro Lys Met Gly Met Leu Lys Arg Arg Ile Met Pro Glu Asp Ile			
370	375	380	
atc atc aac tgt agc aaa gat gcc aag gtt cct tct cct cca gga			1440
Ile Ile Asn Cys Ser Lys Asp Ala Lys Val Pro Ser Pro Pro Gly			
385	390	395	
cat aag tgg aaa gaa gtc cgg cat gat aac aag gtt act tgg ctg gtt			1488
His Lys Trp Lys Glu Val Arg His Asp Asn Lys Val Thr Trp Leu Val			
400	405	410	
tcc tgg aca gag aac atc caa ggt tcc att aaa tac atc atg ctt aac			1536
Ser Trp Thr Glu Asn Ile Gln Gly Ser Ile Lys Tyr Ile Met Leu Asn			
415	420	425	430
cct agt tca cga atc aag ggt gag aag gac tgg cag aaa tac gag act			1584
Pro Ser Ser Arg Ile Lys Gly Glu Lys Asp Trp Gln Lys Tyr Glu Thr			
435	440	445	
gct cgg cgg ctg aaa aaa tgt gtg gac aag atc cgg aac cag tat cga			1632
Ala Arg Arg Leu Lys Lys Cys Val Asp Lys Ile Arg Asn Gln Tyr Arg			
450	455	460	
gaa gac tgg aag tcc aaa gag atg aaa gtc cgg cag aca gct gta gcc			1680
Glu Asp Trp Lys Ser Lys Glu Met Lys Val Arg Gln Arg Ala Val Ala			
465	470	475	
ctg tac ttc atc gac aag ctt gct ctg aga gca ggc aat gaa aag gag			1728
Leu Tyr Phe Ile Asp Lys Leu Ala Leu Arg Ala Gly Asn Glu Lys Glu			
480	485	490	
gaa gga gaa aca gcg gac act gtg ggc tgc tgc tca ctt cgt gtg gag			1776
Glu Gly Glu Thr Ala Asp Thr Val Gly Cys Cys Ser Leu Arg Val Glu			

495	500	505	510	
cac atc aat cta cac cca gag ttg gat ggt cag gaa tat gtg gta gag				1824
His Ile Asn Leu His Pro Glu Leu Asp Gly Gln Glu Tyr Val Val Glu				
515	520	525		
ttt gac ttc ctc ggg aag gac tcc atc aga tac tat aac aag gtc cct				1872
Phe Asp Phe Leu Gly Lys Asp Ser Ile Arg Tyr Tyr Asn Lys Val Pro				
530	535	540		
gtt gag aaa cga gtt ttt aag aac cta caa cta ttt atg gag aac aag				1920
Val Glu Lys Arg Val Phe Lys Asn Leu Gln Leu Phe Met Glu Asn Lys				
545	550	555		
cag ccc gag gat gat ctt ttt gat aga ctc aat act ggt att ctg aat				1968
Gln Pro Glu Asp Asp Leu Phe Asp Arg Leu Asn Thr Gly Ile Leu Asn				
560	565	570		
aag cat ctt cag gat ctc atg gag ggc ttg aca gcc aag gta ttc cgt				2016
Lys His Leu Gln Asp Leu Met Glu Gly Leu Thr Ala Lys Val Phe Arg				
575	580	585	590	
aca tac aat gcc tcc atc acg cta cag cag cag cta aaa gaa ctg aca				2064
Thr Tyr Asn Ala Ser Ile Thr Leu Gln Gln Leu Lys Glu Leu Thr				
595	600	605		
gcc ccg gat gag aac atc cca gcg aag atc ctt tct tat aac cgt gcc				2112
Ala Pro Asp Glu Asn Ile Pro Ala Lys Ile Leu Ser Tyr Asn Arg Ala				
610	615	620		
aat cga gct gtt gca att ctt tgt aac cat cag agg gca cca cca aaa				2160
Asn Arg Ala Val Ala Ile Leu Cys Asn His Gln Arg Ala Pro Pro Lys				
625	630	635		
act ttt gag aag tct atg aac ttg caa act aag att gat gcc aag				2208
Thr Phe Glu Lys Ser Met Met Asn Leu Gln Thr Lys Ile Asp Ala Lys				
640	645	650		
aag gaa cag cta gca gat gcc cgg aga gac ctg aaa agt gct aag gct				2256
Lys Glu Gln Leu Ala Asp Ala Arg Arg Asp Leu Lys Ser Ala Lys Ala				
655	660	665	670	
gat gcc aag gtc atg aag gat gca aag acg aag aag gta gta gag tca				2304
Asp Ala Lys Val Met Lys Asp Ala Lys Thr Lys Lys Val Val Glu Ser				
675	680	685		
aag aag aag gct gtt cag aga ctg gag gaa cag gag ttg atg aag ctg gaa				2352
Lys Lys Lys Ala Val Gln Arg Leu Glu Glu Gln Leu Met Lys Leu Glu				
690	695	700		
gtt caa gcc aca gac cga gag gaa aat aaa cag att gcc ctg gga acc				2400
Val Gln Ala Thr Asp Arg Glu Glu Asn Lys Gln Ile Ala Leu Gly Thr				
705	710	715		

100	105	110
Pro Pro Gln Ile Lys Asp Glu Pro	Glu Asp Asp Gly Tyr	Phe Val Pro
115	120	125
Pro Lys Glu Asp Ile Lys Pro	Leu Lys Arg Pro Arg Asp Glu Asp Asp	
130	135	140
Ala Asp Tyr Lys Pro Lys Lys	Ile Lys Thr Glu Asp Thr Lys Lys Glu	
145	150	155
Lys Lys Arg Lys Leu Glu Glu	Glu Asp Gly Lys Leu Lys Pro	
165	170	175
Lys Asn Lys Asp Lys Asp Lys Lys	Val Pro Glu Pro Asp Asn Lys Lys	
180	185	190
Lys Lys Pro Lys Lys Glu Glu	Gln Lys Trp Lys Trp Trp Glu Glu	
195	200	205
Glu Arg Tyr Pro Glu Gly Ile Lys Trp	Lys Phe Leu Glu His Lys Gly	
210	215	220
Pro Val Phe Ala Pro Pro Tyr Glu	Pro Leu Pro Glu Asn Val Lys Phe	
225	230	235
Tyr Tyr Asp Gly Lys Val Met Lys	Leu Ser Pro Lys Ala Glu Glu Val	
245	250	255
Ala Thr Phe Phe Ala Lys Met Leu	Asp His Glu Tyr Thr Thr Lys Glu	
260	265	270
Ile Phe Arg Lys Asn Phe Phe Lys	Asp Trp Arg Lys Glu Met Thr Asn	
275	280	285
Glu Glu Lys Asn Ile Ile Thr Asn	Leu Ser Lys Cys Asp Phe Thr Gln	
290	295	300
Met Ser Gln Tyr Phe Lys Ala Gln	Thr Glu Ala Arg Lys Gln Met Ser	
305	310	315
Lys Glu Glu Lys Leu Lys Ile Lys	Glu Asn Glu Lys Leu Leu Lys	
325	330	335
Glu Tyr Gly Phe Cys Ile Met Asp	Asn His Lys Glu Arg Ile Ala Asn	
340	345	350
Phe Lys Ile Glu Pro Pro Gly Leu	Phe Arg Gly Arg Gly Asn His Pro	
355	360	365
Lys Met Gly Met Leu Lys Arg Arg	Ile Met Pro Glu Asp Ile Ile Ile	
370	375	380
Asn Cys Ser Lys Asp Ala Lys Val	Pro Ser Pro Pro Gly His Lys	
385	390	395
Trp Lys Glu Val Arg His Asp Asn	Lys Val Thr Trp Leu Val Ser Trp	
405	410	415
Thr Glu Asn Ile Gln Gly Ser Ile	Lys Tyr Ile Met Leu Asn Pro Ser	
420	425	430
Ser Arg Ile Lys Gly Glu Lys	Asp Trp Gln Lys Tyr Glu Thr Ala Arg	
435	440	445
Arg Leu Lys Lys Cys Val Asp Lys	Ile Arg Asn Gln Tyr Arg Glu Asp	
450	455	460
Trp Lys Ser Lys Glu Met Lys Val	Arg Gln Arg Ala Val Ala Leu Tyr	
465	470	475
Phe Ile Asp Lys Leu Ala Leu Arg	Ala Gly Asn Glu Lys Glu Glu Gly	
485	490	495
Glu Thr Ala Asp Thr Val Gly Cys	Cys Ser Leu Arg Val Glu His Ile	
500	505	510
Asn Leu His Pro Glu Leu Asp Gly	Gln Glu Tyr Val Val Glu Phe Asp	
515	520	525

Phe Leu Gly Lys Asp Ser Ile Arg Tyr Tyr Asn Lys Val Pro Val Glu
530 535 540
Lys Arg Val Phe Lys Asn Leu Gln Leu Phe Met Glu Asn Lys Gln Pro
545 550 555 560
Glu Asp Asp Leu Phe Asp Arg Leu Asn Thr Gly Ile Leu Asn Lys His
565 570 575
Leu Gln Asp Leu Met Glu Gly Leu Thr Ala Lys Val Phe Arg Thr Tyr
580 585 590
Asn Ala Ser Ile Thr Leu Gln Gln Leu Lys Glu Leu Thr Ala Pro
595 600 605
Asp Glu Asn Ile Pro Ala Lys Ile Leu Ser Tyr Asn Arg Ala Asn Arg
610 615 620
Ala Val Ala Ile Leu Cys Asn His Gln Arg Ala Pro Pro Lys Thr Phe
625 630 635 640
Glu Lys Ser Met Met Asn Leu Gln Thr Lys Ile Asp Ala Lys Lys Glu
645 650 655
Gln Leu Ala Asp Ala Arg Arg Asp Leu Lys Ser Ala Lys Ala Asp Ala
660 665 670
Lys Val Met Lys Asp Ala Lys Thr Lys Lys Val Val Glu Ser Lys Lys
675 680 685
Lys Ala Val Gln Arg Leu Glu Glu Gln Leu Met Lys Leu Glu Val Gln
690 695 700
Ala Thr Asp Arg Glu Glu Asn Lys Gln Ile Ala Leu Gly Thr Ser Lys
705 710 715 720
Leu Asn Tyr Leu Asp Pro Arg Ile Thr Val Ala Trp Cys Lys Lys Trp
725 730 735
Gly Val Pro Ile Glu Lys Ile Tyr Asn Lys Thr Gln Arg Glu Lys Phe
740 745 750
Ala Trp Ala Ile Asp Met Ala Asp Glu Asp Tyr Glu Phe
755 760 765

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<221> CDS
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cac atc gaa ggt cgt atc aag tgg aaa ttc cta gaa cat aaa ggt cca 96
His Ile Glu Gly Arg Ile Lys Trp Lys Phe Leu Glu His Lys Gly Pro
20 25 30

gta ttt gcc cca cca tat gag cct ctt cca gag aat gtc aag ttt tat 144

Val Phe Ala Pro Pro Tyr Glu Pro Leu Pro Glu Asn Val Lys Phe Tyr			
35	40	45	
tat gat ggt aaa gtc atg aag ctg agc ccc aaa gca gag gaa gta gct			192
Tyr Asp Gly Lys Val Met Lys Leu Ser Pro Lys Ala Glu Glu Val Ala			
50	55	60	
acg ttc ttt gca aaa atg ctc gac cat gaa tat act acc aag gaa ata			240
Thr Phe Phe Ala Lys Met Leu Asp His Glu Tyr Thr Lys Glu Ile			
65	70	75	80
ttt agg aaa aat ttc ttt aaa gac tgg aga aag gaa atg act aat gaa			288
Phe Arg Lys Asn Phe Phe Lys Asp Trp Arg Lys Glu Met Thr Asn Glu			
85	90	95	
gag aag aat att atc acc aac cta agc aaa tgt gat ttt acc cag atg			336
Glu Lys Asn Ile Ile Thr Asn Leu Ser Lys Cys Asp Phe Thr Gln Met			
100	105	110	
agc cag tat ttc aaa gcc cag acg gaa gct cgg aaa cag atg agc aag			384
Ser Gln Tyr Phe Lys Ala Gln Thr Glu Ala Arg Lys Gln Met Ser Lys			
115	120	125	
gaa gag aaa ctg aaa atc aaa gag gag aat gaa aaa tta ctg aaa gaa			432
Glu Glu Lys Leu Lys Ile Lys Glu Glu Asn Glu Lys Leu Leu Lys Glu			
130	135	140	
tat gga ttc tgt att atg gat aac cac aaa gag agg att gct aac ttc			480
Tyr Gly Phe Cys Ile Met Asp Asn His Lys Glu Arg Ile Ala Asn Phe			
145	150	155	160
aag ata gag cct cct gga ctt ttc cgt ggc cgc ggc aac cac ccc aag			528
Lys Ile Glu Pro Pro Gly Leu Phe Arg Gly Arg Gly Asn His Pro Lys			
165	170	175	
atg ggc atg ctg aag aga cga atc atg ccc gag gat ata atc atc aac			576
Met Gly Met Leu Lys Arg Arg Ile Met Pro Glu Asp Ile Ile Asn			
180	185	190	
tgt agc aaa gat gcc aag gtt cct tct cct cca gga cat aag tgg			624
Cys Ser Lys Asp Ala Lys Val Pro Ser Pro Pro Gly His Lys Trp			
195	200	205	
aaa gaa gtc cgg cat gat aac aag gtt act tgg ctg gtt tcc tgg aca			672
Lys Glu Val Arg His Asp Asn Lys Val Thr Trp Leu Val Ser Trp Thr			
210	215	220	
gag aac atc caa ggt tcc att aaa tac atc atg ctt aac cct agt tca			720
Glu Asn Ile Gln Gly Ser Ile Lys Tyr Ile Met Leu Asn Pro Ser Ser			
225	230	235	240
cga atc aag ggt gag aag gac tgg cag aaa tac gag act gct cgg cgg			768
Arg Ile Lys Gly Glu Lys Asp Trp Gln Lys Tyr Glu Thr Ala Arg Arg			

245

250

255

ctg aaa aaa tgt gtg gac aag atc cg^g aac cag tat cga gaa gac tgg 816
Leu Lys Lys Cys Val Asp Lys Ile Arg Asn Gln Tyr Arg Glu Asp Trp
260 265 270

aag tcc aaa gag atg aaa gtc cg^g cag aga gct gta gcc ctg tac ttc 864
Lys Ser Lys Glu Met Lys Val Arg Gln Arg Ala Val Ala Leu Tyr Phe
275 280 285

atc gac aag ctt gct ctg aga gca ggc aat gaa aag gag gaa gga gaa 912
Ile Asp Lys Leu Ala Leu Arg Ala Gly Asn Glu Lys Glu Glu Gly Glu
290 295 300

aca ggc gac act gtg ggc tgc tgc tca ctt cgt gtg gag cac atc aat 960
Thr Ala Asp Thr Val Gly Cys Ser Leu Arg Val Glu His Ile Asn
305 310 315 320

cta cac cca gag ttg gat ggt cag gaa tat gtg gta gag ttt gac ttc 1008
Leu His Pro Glu Leu Asp Gly Gln Glu Tyr Val Val Glu Phe Asp Phe
325 330 335

ctc ggg aag gac tcc atc aga tac tat aac aag gtc cct gtt gag aaa 1056
Leu Gly Lys Asp Ser Ile Arg Tyr Tyr Asn Lys Val Pro Val Glu Lys
340 345 350

cga gtt ttt aag aac cta caa cta ttt atg gag aac aag cag ccc gag 1104
Arg Val Phe Lys Asn Leu Gln Leu Phe Met Glu Asn Lys Gln Pro Glu
355 360 365

gat gat ctt ttt gat aga ctc aat act ggt att ctg aat aag cat ctt 1152
Asp Asp Leu Phe Asp Arg Leu Asn Thr Gly Ile Leu Asn Lys His Leu
370 375 380

cag gat ctc atg gag ggc ttg aca gcc aag gta ttc cgt acg tac aat 1200
Gln Asp Leu Met Glu Gly Leu Thr Ala Lys Val Phe Arg Thr Tyr Asn
385 390 395 400

gcc tcc atc acg cta cag cag cta aaa gaa ctg aca gcc ccg gat 1248
Ala Ser Ile Thr Leu Gln Gln Leu Lys Glu Leu Thr Ala Pro Asp
405 410 415

gag aac atc cca gcg aag atc ctt tct tat aac cgt gcc aat cga gct 1296
Glu Asn Ile Pro Ala Lys Ile Leu Ser Tyr Asn Arg Ala Asn Arg Ala
420 425 430

gtt gca att cct tgt aac cat cag agg gca cca aaa act ttt gag 1344
Val Ala Ile Leu Cys Asn His Gln Arg Ala Pro Pro Lys Thr Phe Glu
435 440 445

aag tct atg atg aac ttg caa act aag att gat gcc aag aag gaa cag 1392
Lys Ser Met Met Asn Leu Gln Thr Lys Ile Asp Ala Lys Lys Glu Gln
450 455 460

cta gca gat gcc cgg aga gac gtc aaa agt gct aag gtc gat gcc aag 1440
Leu Ala Asp Ala Arg Arg Asp Leu Lys Ser Ala Lys Ala Asp Ala Lys
465 470 475 480

gtc atg aag gat gca aag acg aag aag gta gta gag tca aag aag aag 1488
Val Met Lys Asp Ala Lys Thr Lys Lys Val Val Glu Ser Lys Lys
485 490 495

gct gtt cag aga ctg gag gaa cag ttg atg aag ctg gaa gtt caa gcc 1536
Ala Val Gln Arg Leu Glu Glu Gln Leu Met Lys Leu Glu Val Gln Ala
500 505 510

aca gac cga gag gaa aat aaa cag att gcc ctg gga acc tcc aaa ctc 1584
Thr Asp Arg Glu Glu Asn Lys Gln Ile Ala Leu Gly Thr Ser Lys Leu
515 520 525

aat tat ctg gac cct agg atc aca gtg gct tgg tgc aag aag tgg ggt 1632
Asn Tyr Leu Asp Pro Arg Ile Thr Val Ala Trp Cys Lys Lys Trp Gly
530 535 540

gtc cca att gag aag att tac aac aaa acc cag cgg gag aag ttt gcc 1680
Val Pro Ile Glu Lys Ile Tyr Asn Lys Thr Gln Arg Glu Lys Phe Ala
545 550 555 560

tgg gcc att gag atg gct gat gaa gac tat gag ttt tag 1719
Trp Ala Ile Asp Met Ala Asp Glu Asp Tyr Glu Phe
565 570

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<212> PRT
<213> Artificial Sequence

<220>
<223> human fusion

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His Ile Glu Gly Arg Ile Lys Trp Lys Phe Leu Glu His Lys Gly Pro
20 25 30
Val Phe Ala Pro Pro Tyr Glu Pro Leu Pro Glu Asn Val Lys Phe Tyr
35 40 45
Tyr Asp Gly Lys Val Met Lys Leu Ser Pro Lys Ala Glu Glu Val Ala
50 55 60
Thr Phe Phe Ala Lys Met Leu Asp His Glu Tyr Thr Thr Lys Glu Ile
65 70 75 80
Phe Arg Lys Asn Phe Phe Lys Asp Trp Arg Lys Glu Met Thr Asn Glu
85 90 95
Glu Lys Asn Ile Ile Thr Asn Leu Ser Lys Cys Asp Phe Thr Gln Met
100 105 110

Ser Gln Tyr Phe Lys Ala Gln Thr Glu Ala Arg Lys Gln Met Ser Lys
115 120 125
Glu Glu Lys Leu Lys Ile Lys Glu Glu Asn Glu Lys Leu Leu Lys Glu
130 135 140
Tyr Gly Phe Cys Ile Met Asp Asn His Lys Glu Arg Ile Ala Asn Phe
145 150 155 160
Lys Ile Glu Pro Pro Gly Leu Phe Arg Gly Arg Gly Asn His Pro Lys
165 170 175
Met Gly Met Leu Lys Arg Arg Ile Met Pro Glu Asp Ile Ile Asn
180 185 190
Cys Ser Lys Asp Ala Lys Val Pro Ser Pro Pro Gly His Lys Trp
195 200 205
Lys Glu Val Arg His Asp Asn Lys Val Thr Trp Leu Val Ser Trp Thr
210 215 220
Glu Asn Ile Gln Gly Ser Ile Lys Tyr Ile Met Leu Asn Pro Ser Ser
225 230 235 240
Arg Ile Lys Gly Glu Lys Asp Trp Gln Lys Tyr Glu Thr Ala Arg Arg
245 250 255
Leu Lys Lys Cys Val Asp Lys Ile Arg Asn Gln Tyr Arg Glu Asp Trp
260 265 270
Lys Ser Lys Glu Met Lys Val Arg Gln Arg Ala Val Ala Leu Tyr Phe
275 280 285
Ile Asp Lys Leu Ala Leu Arg Ala Gly Asn Glu Lys Glu Glu Gly Glu
290 295 300
Thr Ala Asp Thr Val Gly Cys Cys Ser Leu Arg Val Glu His Ile Asn
305 310 315 320
Leu His Pro Glu Leu Asp Gly Gln Glu Tyr Val Val Glu Phe Asp Phe
325 330 335
Leu Gly Lys Asp Ser Ile Arg Tyr Tyr Asn Lys Val Pro Val Glu Lys
340 345 350
Arg Val Phe Lys Asn Leu Gln Leu Phe Met Glu Asn Lys Gln Pro Glu
355 360 365
Asp Asp Leu Phe Asp Arg Leu Asn Thr Gly Ile Leu Asn Lys His Leu
370 375 380
Gln Asp Leu Met Glu Gly Leu Thr Ala Lys Val Phe Arg Thr Tyr Asn
385 390 395 400
Ala Ser Ile Thr Leu Gln Gln Gln Leu Lys Glu Leu Thr Ala Pro Asp
405 410 415
Glu Asn Ile Pro Ala Lys Ile Leu Ser Tyr Asn Arg Ala Asn Arg Ala
420 425 430
Val Ala Ile Leu Cys Asn His Gln Arg Ala Pro Pro Lys Thr Phe Glu
435 440 445
Lys Ser Met Met Asn Leu Gln Thr Lys Ile Asp Ala Lys Lys Glu Gln
450 455 460
Leu Ala Asp Ala Arg Arg Asp Leu Lys Ser Ala Lys Ala Asp Ala Lys
465 470 475 480
Val Met Lys Asp Ala Lys Thr Lys Lys Val Val Glu Ser Lys Lys Lys
485 490 495
Ala Val Gln Arg Leu Glu Glu Gln Leu Met Lys Leu Glu Val Gln Ala
500 505 510
Thr Asp Arg Glu Glu Asn Lys Gln Ile Ala Leu Gly Thr Ser Lys Leu
515 520 525
Asn Tyr Leu Asp Pro Arg Ile Thr Val Ala Trp Cys Lys Lys Trp Gly

530	535	540
Val Pro Ile Glu Lys Ile Tyr Asn Lys Thr Gln Arg Glu Lys Phe Ala		
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Trp Ala Ile Asp Met Ala Asp Glu Asp Tyr Glu Phe		560
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<220>
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gycctt

6

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<222> (18)...(19)
<223> n=5-bromo-deoxyuridine

<223> synthetic

<400> 6
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22

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<223> synthetic

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22

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<400> 9
gatcaagtctt ttttgcggcc gcg 23

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